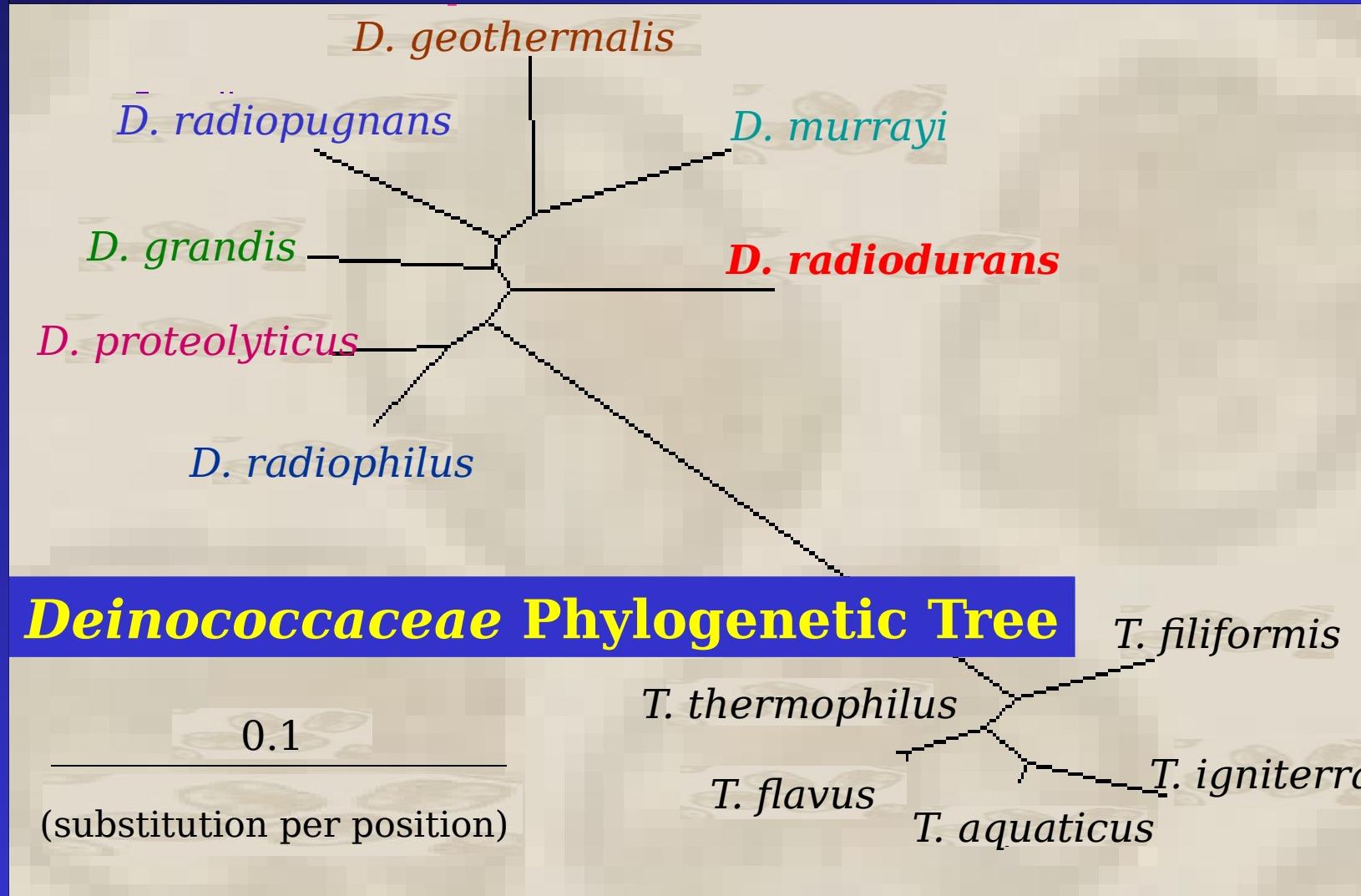
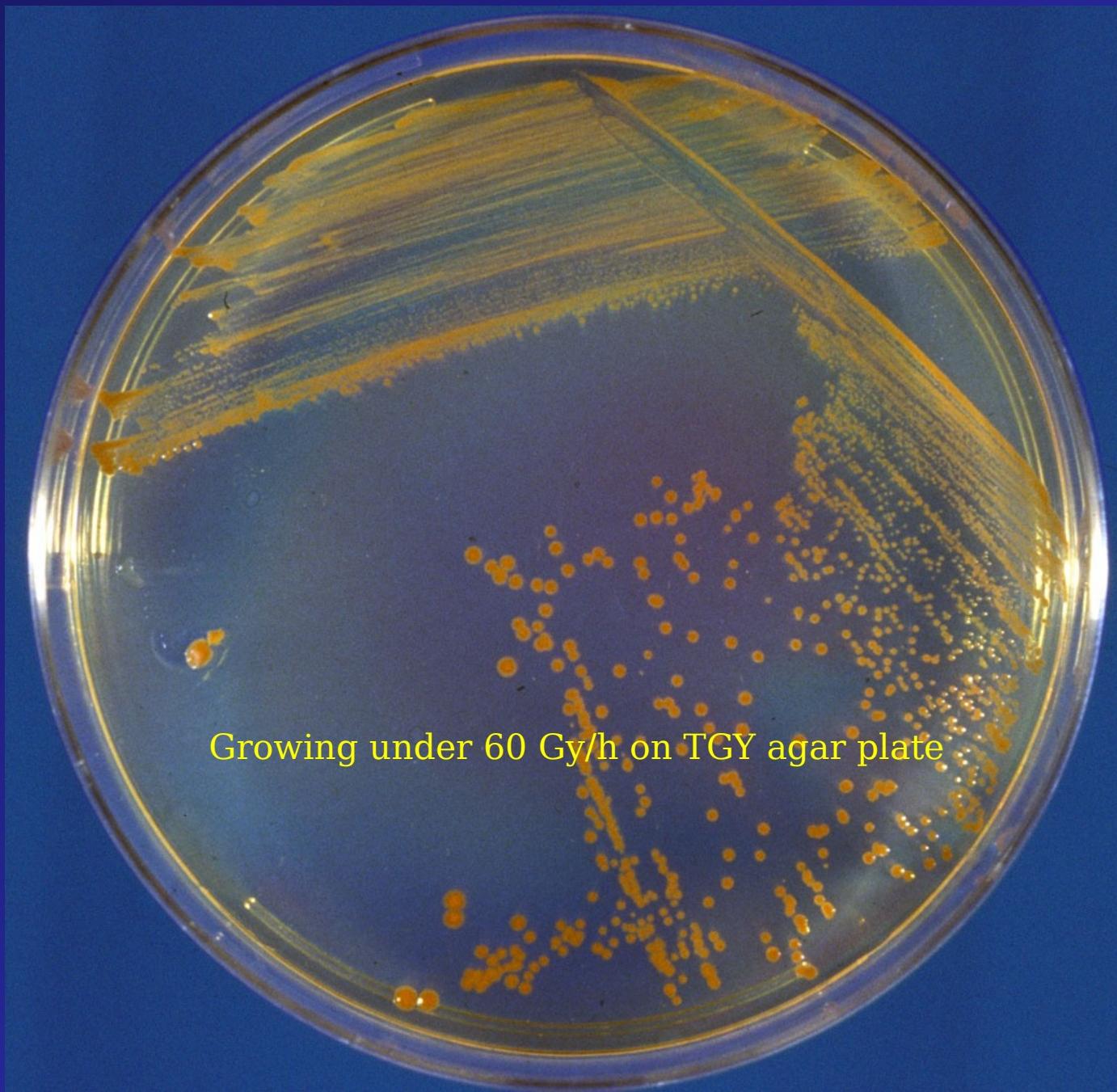


*Deinococcus radiodurans* - a radiation-resistant bacterium



Neighbor-Joining unrooted phylogenetic tree was built using the PHYLIP program on the rRNA sequences. Five *Thermus* species (*T. thermophilus*, *T. flavus*, *T. aquaticus*, *T. igniterrae*) are included as an outgroup. The *Deinococcus/Thermus* group is deeply branched in bacterial trees with putative relationships with the actinobacteria/cyano-bacteria branch. The tree can be found elsewhere (see for example, Wolf et al., BMC Evol. Biol. 2001, Oct 20;1(1):8).

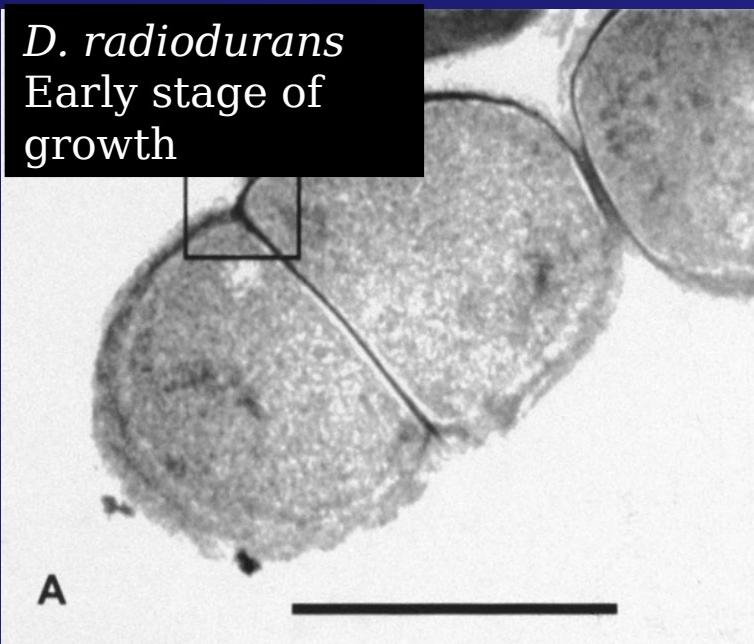
# *D. radiodurans*



Growing under 60 Gy/h on TGY agar plate

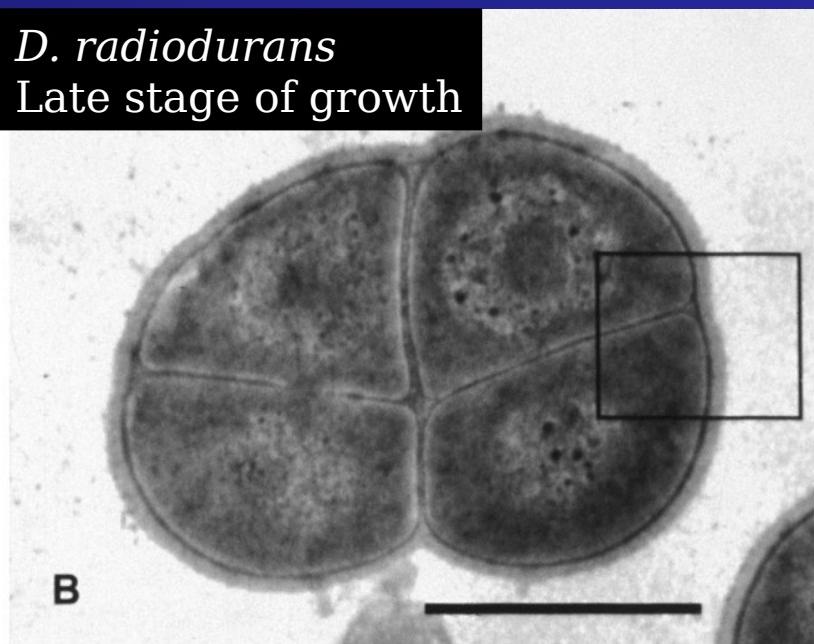
# The Structure of *D. radiodurans*

*D. radiodurans*  
Early stage of  
growth

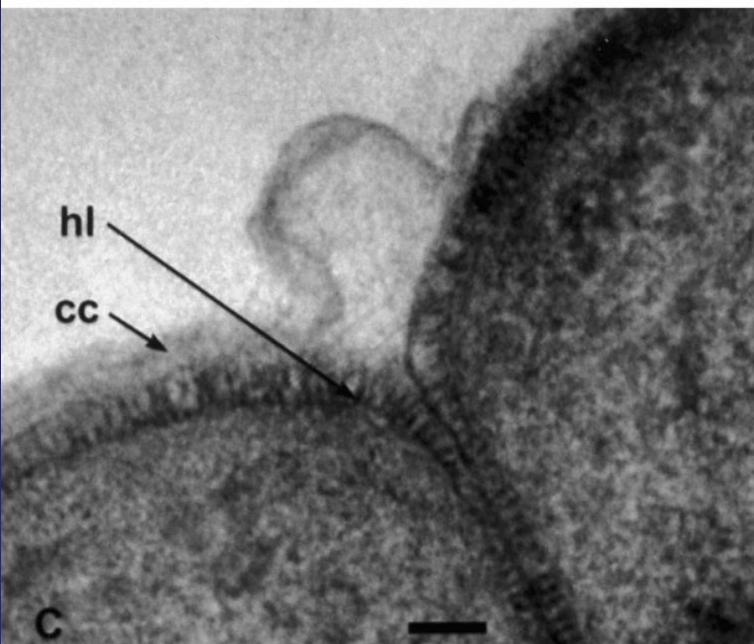


A

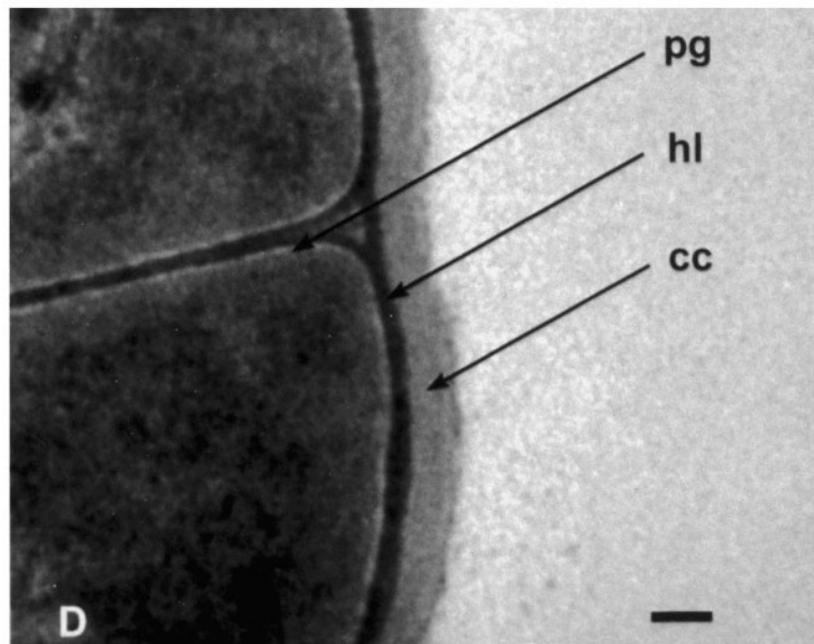
*D. radiodurans*  
Late stage of growth



B

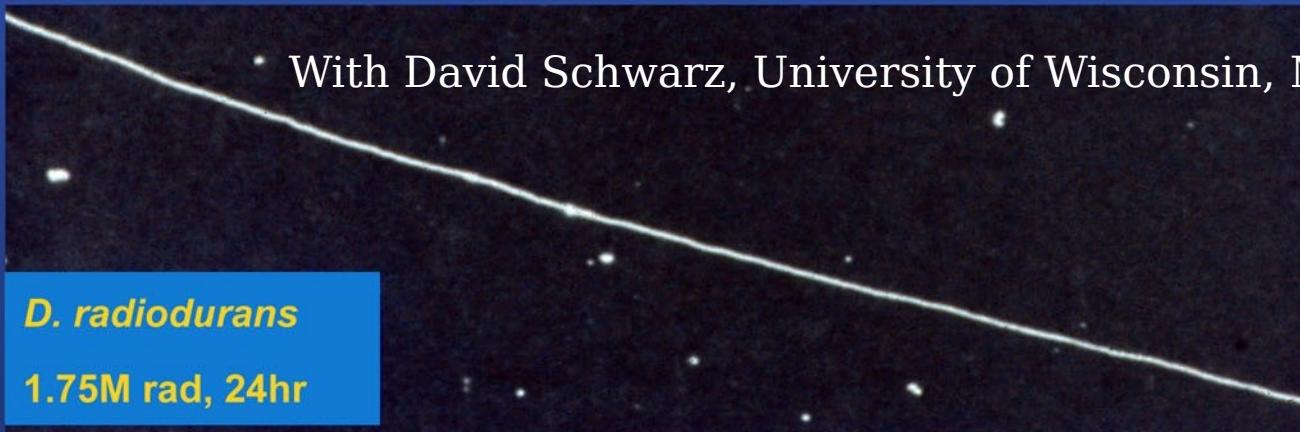
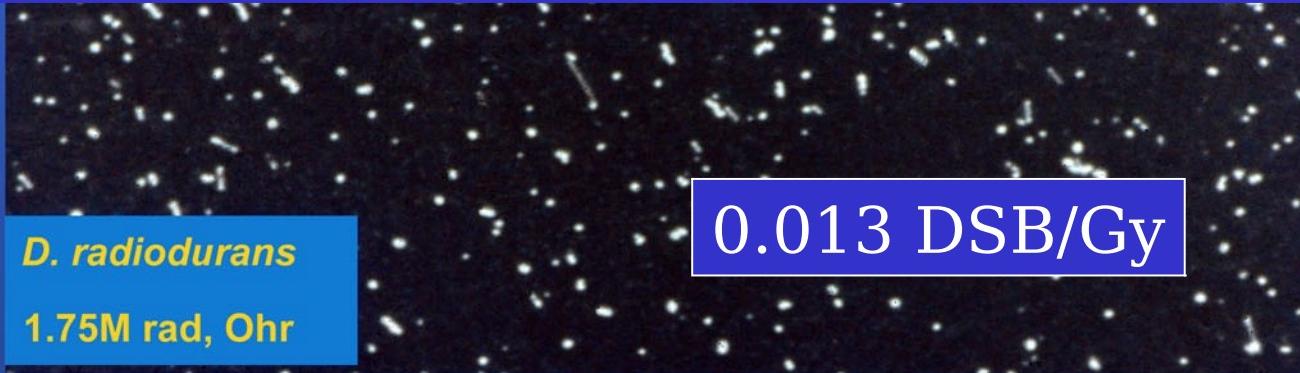


C

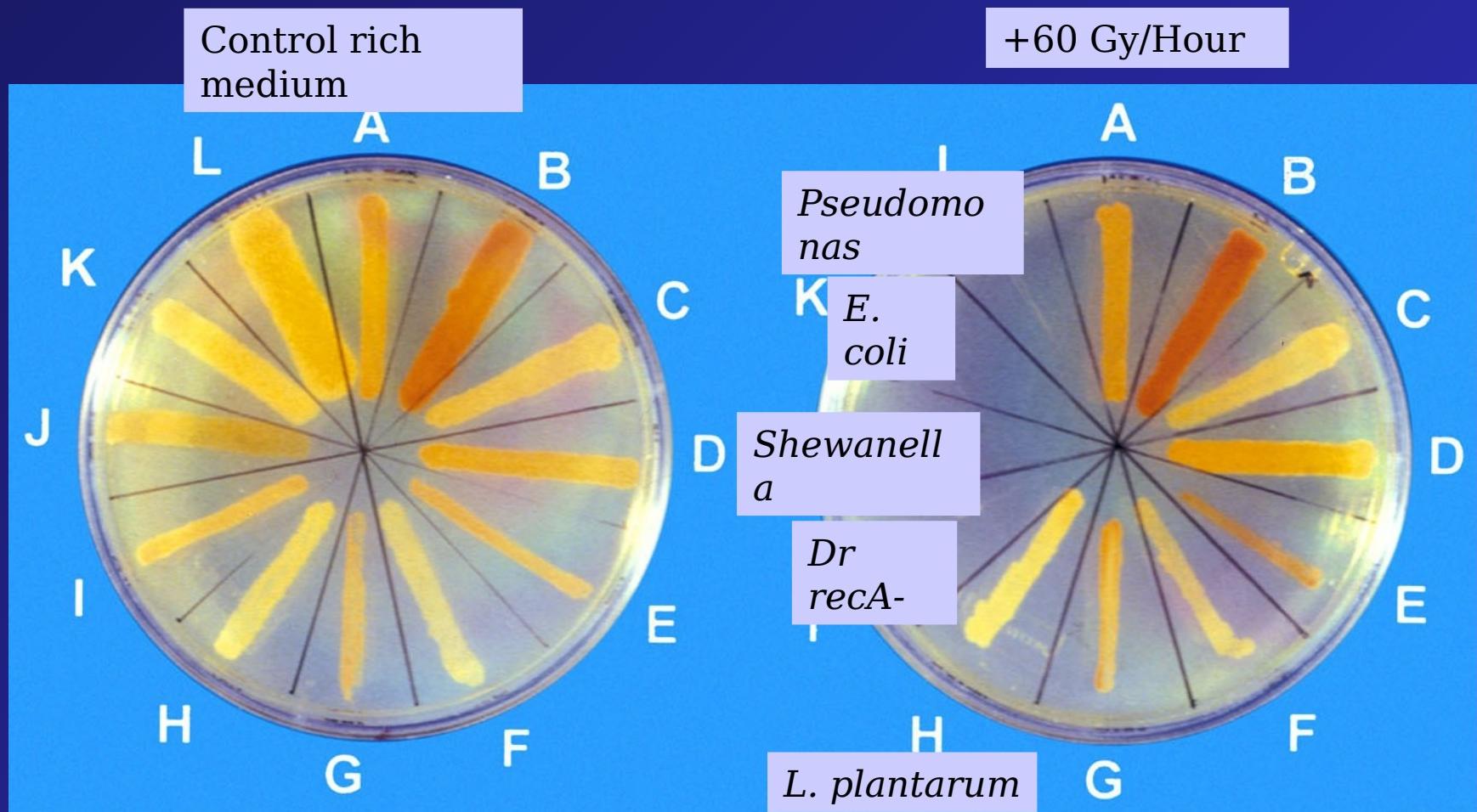


D

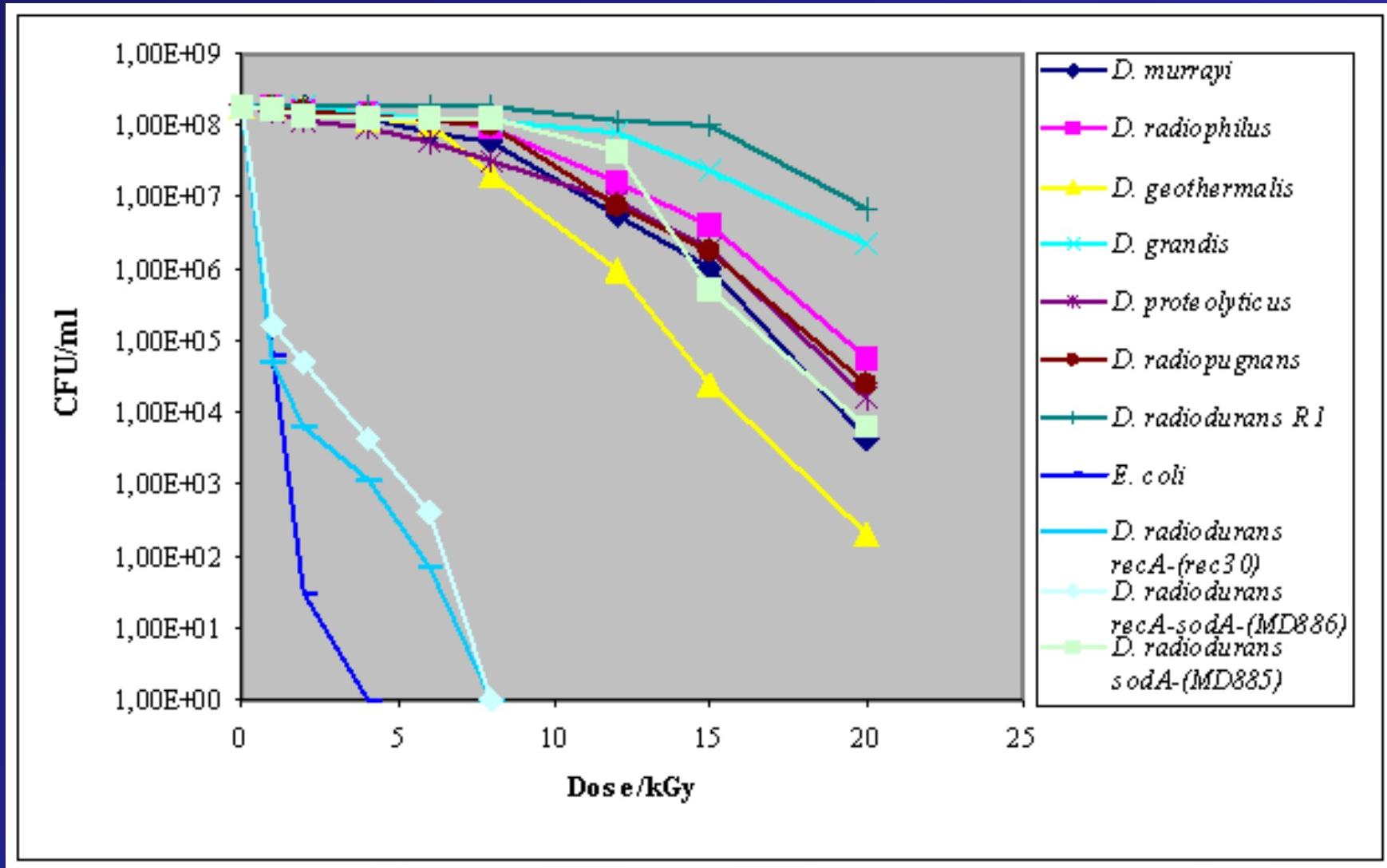
# *D. radiodurans*: The Ultimate DNA Assembly Machine



# Resistance to Chronic Irradiation

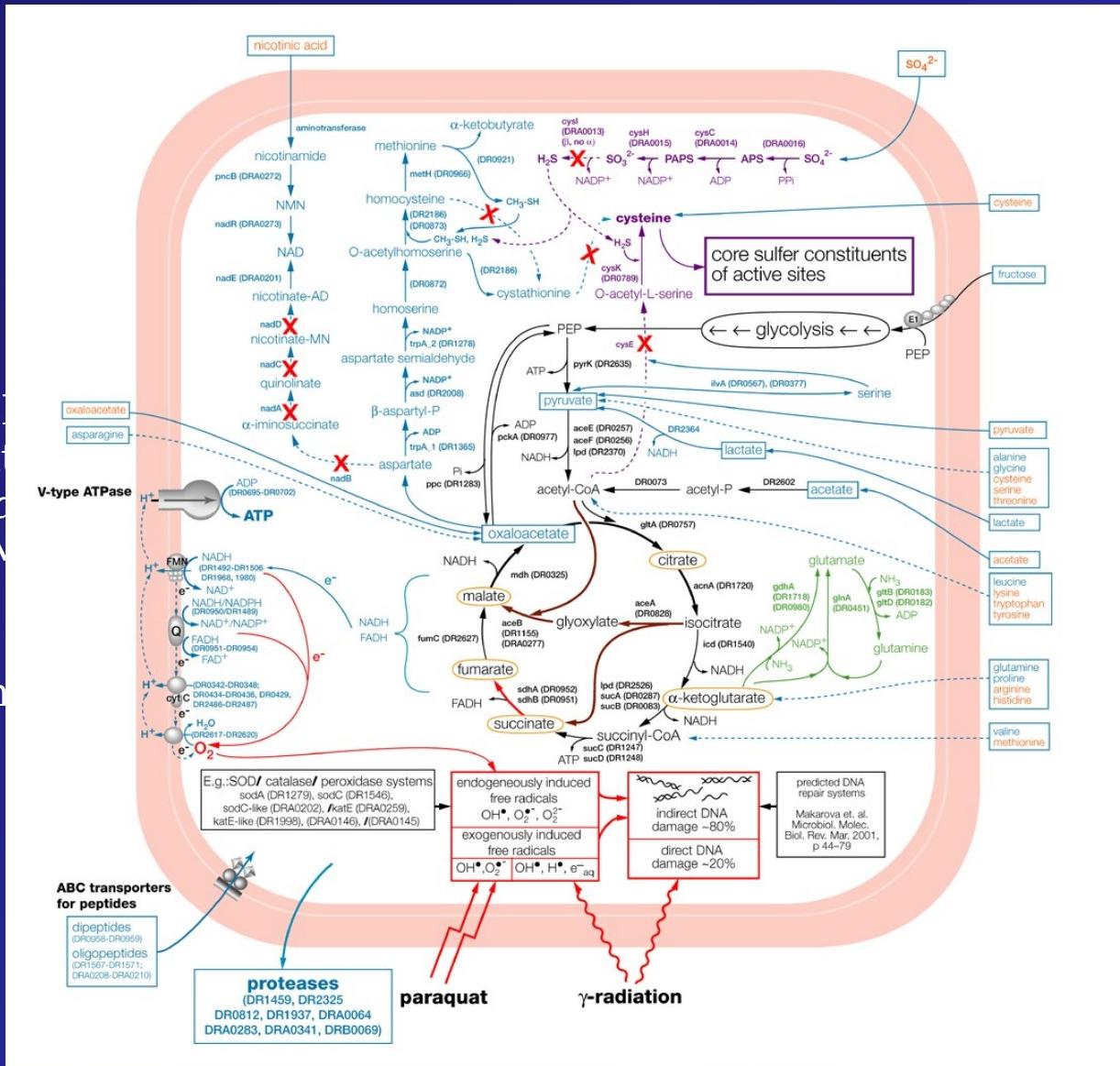


# Resistance to Acute Irradiation



# Predicted *Deinococcus* Metabolic Pathways

Unlike relative radiation sensitive bacteria, *D. radiodurans* recovery on DNA unaffected compared to rich medium



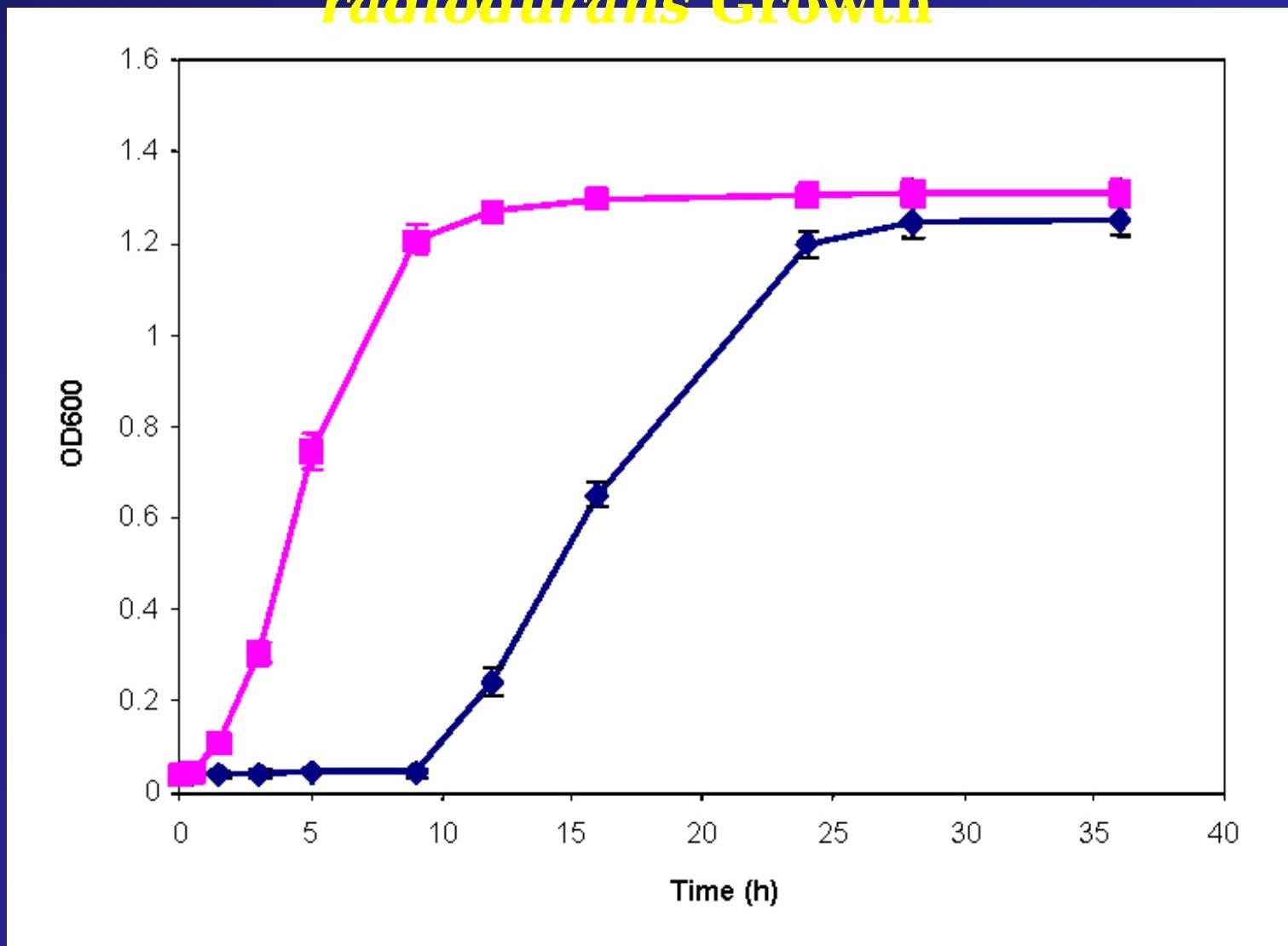
# The lack of a clearly identifiable unique DNA repair system in *D. radiodurans* has given rise to three competing views of the mechanisms responsible for its extraordinary survival

- (i) there are novel repair functions encoded among hypothetical genes predicted by genomic annotation
- (ii) *D. radiodurans* uses conventional DNA repair pathways, but with greater efficiency than other bacteria; or
- (iii) DNA repair in *D. radiodurans* is facilitated by its ringlike chromosomal structures.

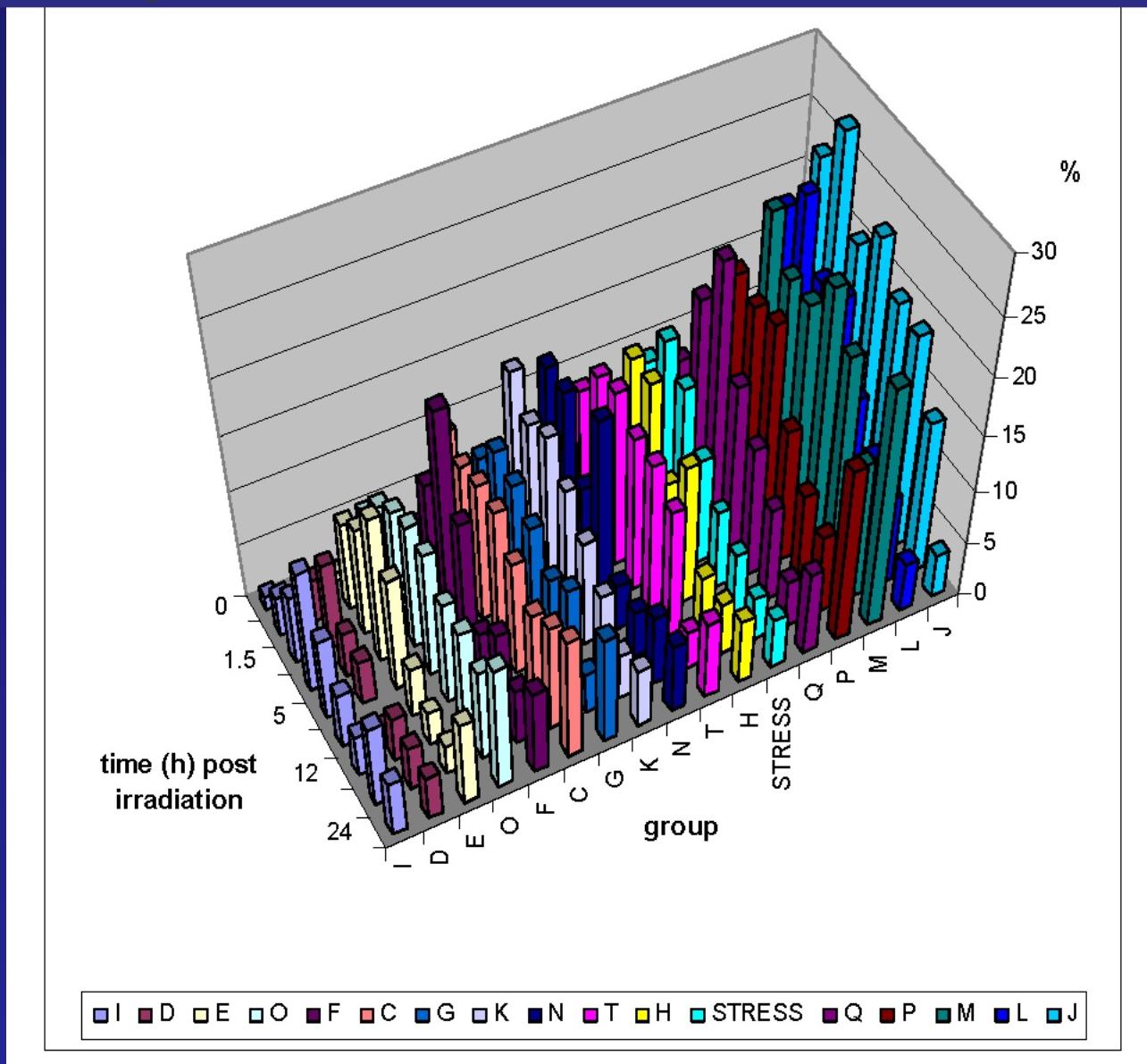
The emphasis of these hypotheses is on DNA repair of irradiation-induced damage, with little consideration given to the possibility that protection against DNA-damage during or after irradiation could be key to recovery.

To read how very muddy the field of understanding is, see 'Unlocking radiation resistance mechanisms: still a long way to go.' Issay Narumi, *Trends in Microbiology* September 2003, p. 422-425,. Also, Edwards J.S. & Battista J.R. *Trends in Biotechnology* September 2003,

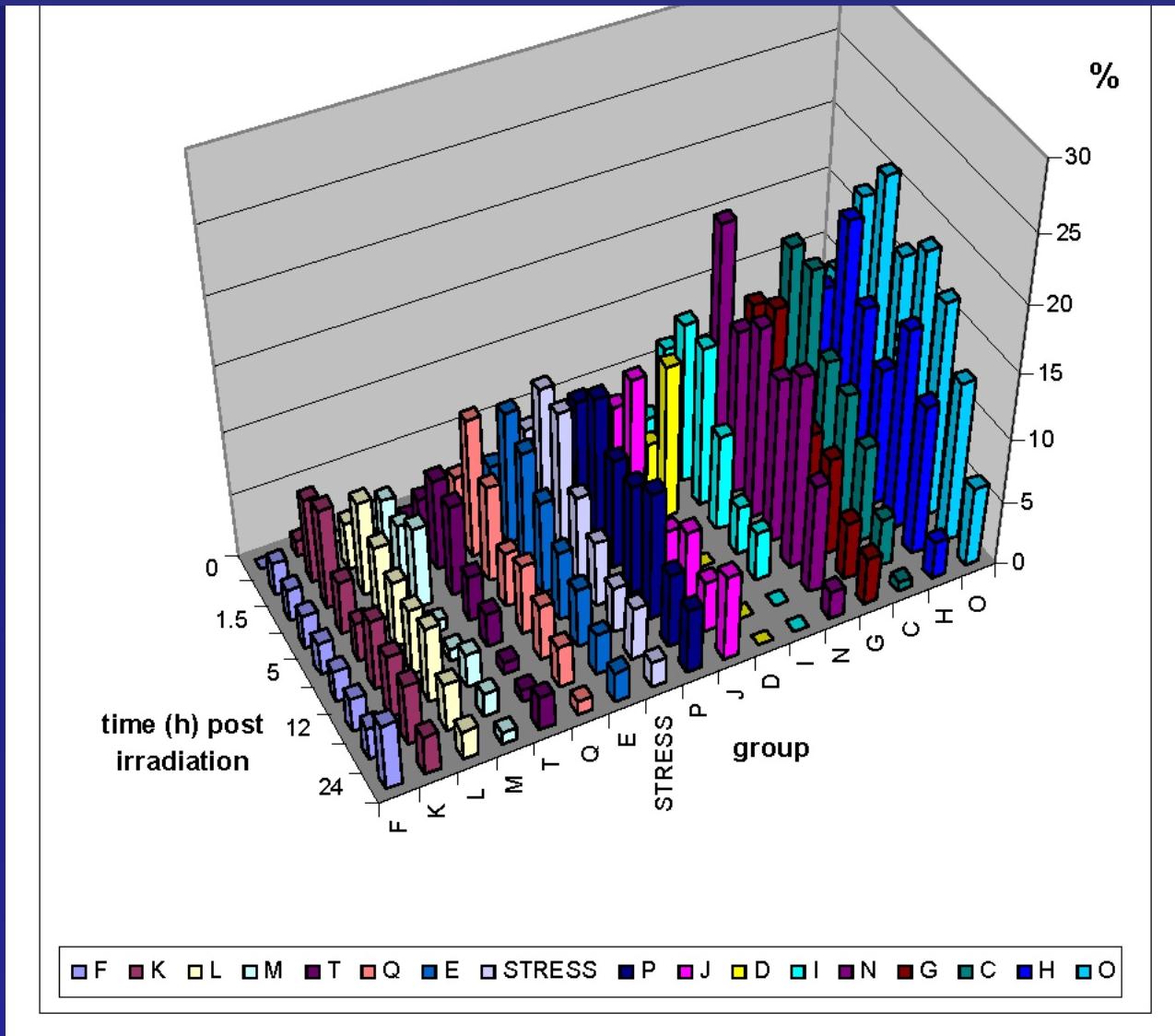
# Effect of High-Dose Acute Irradiation on *D. radiodurans* Growth



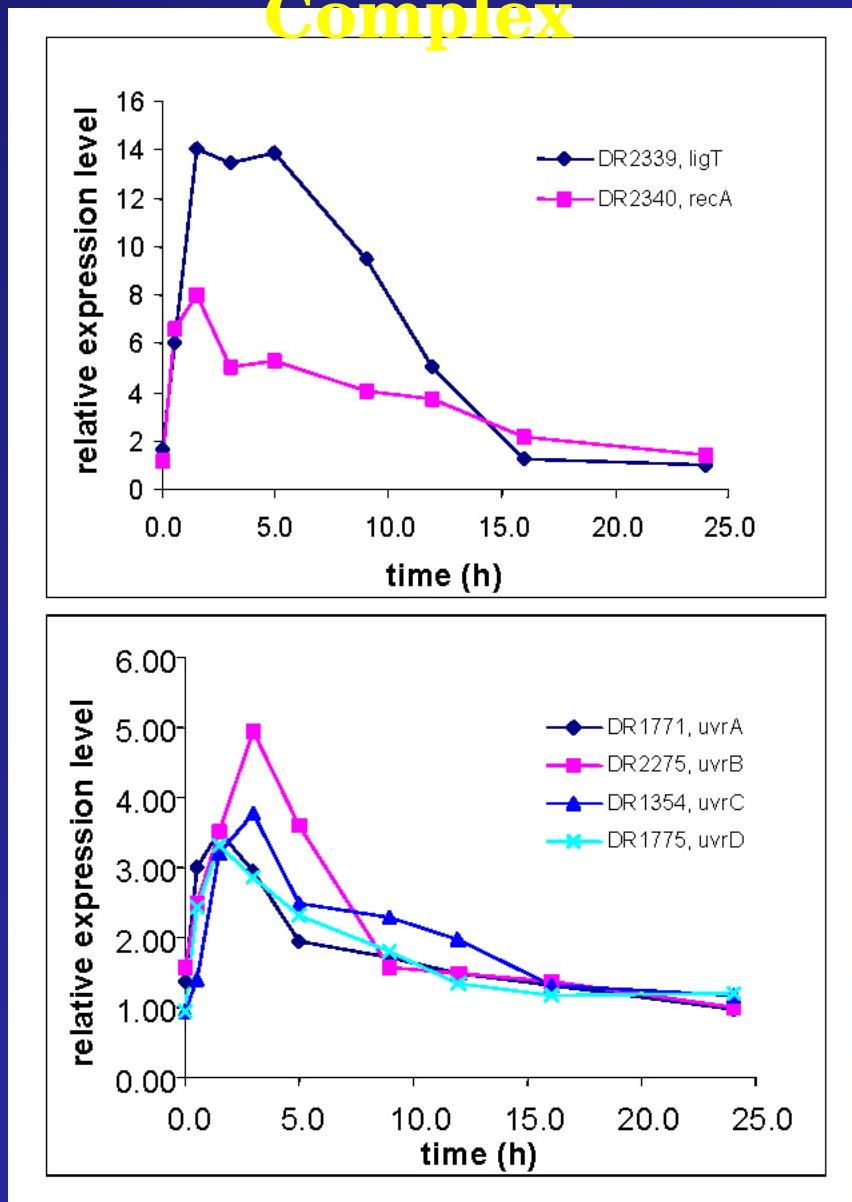
# Up-Regulated Genes in Different Functional Groups



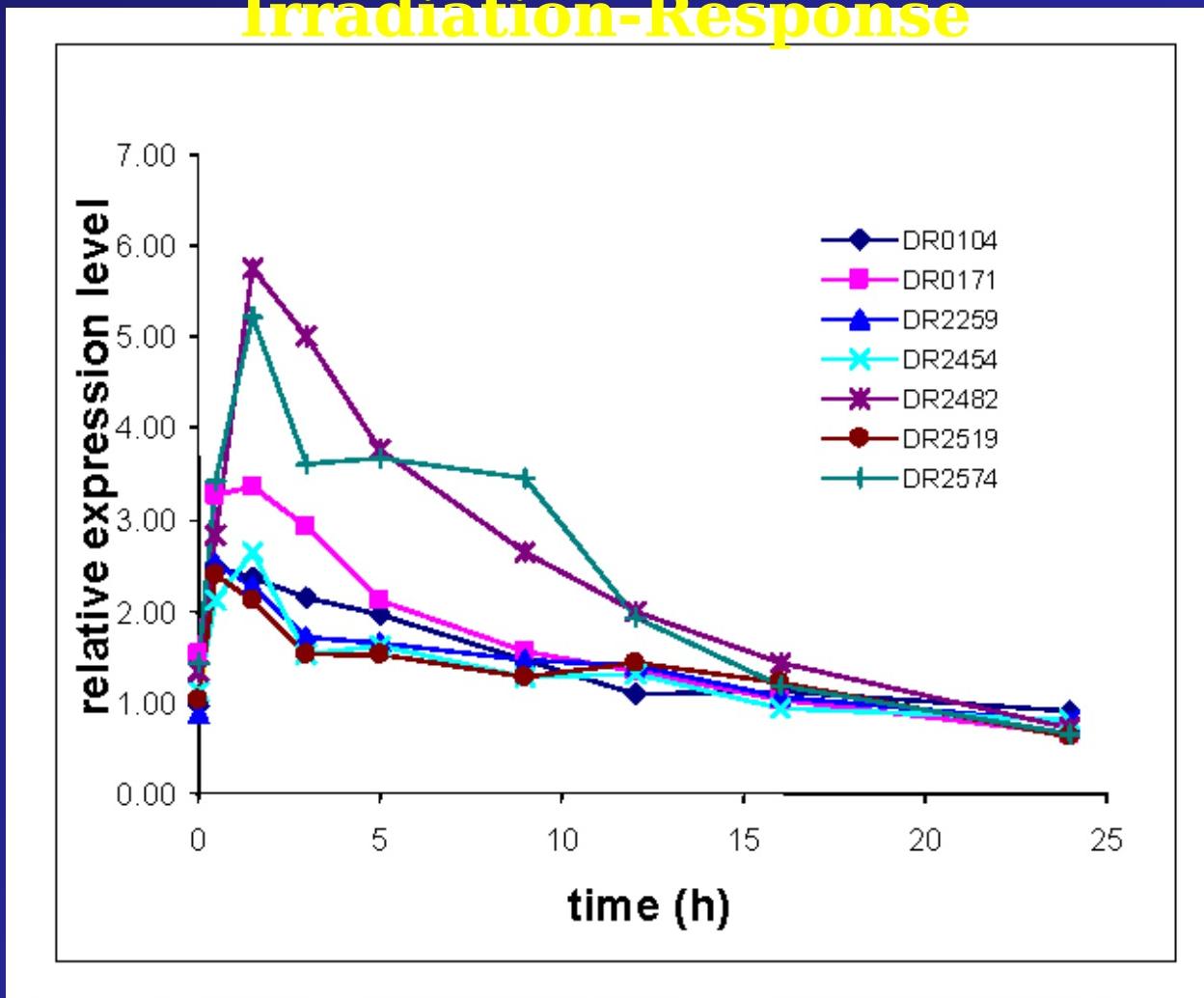
# Down-Regulated Genes in Different Functional Groups



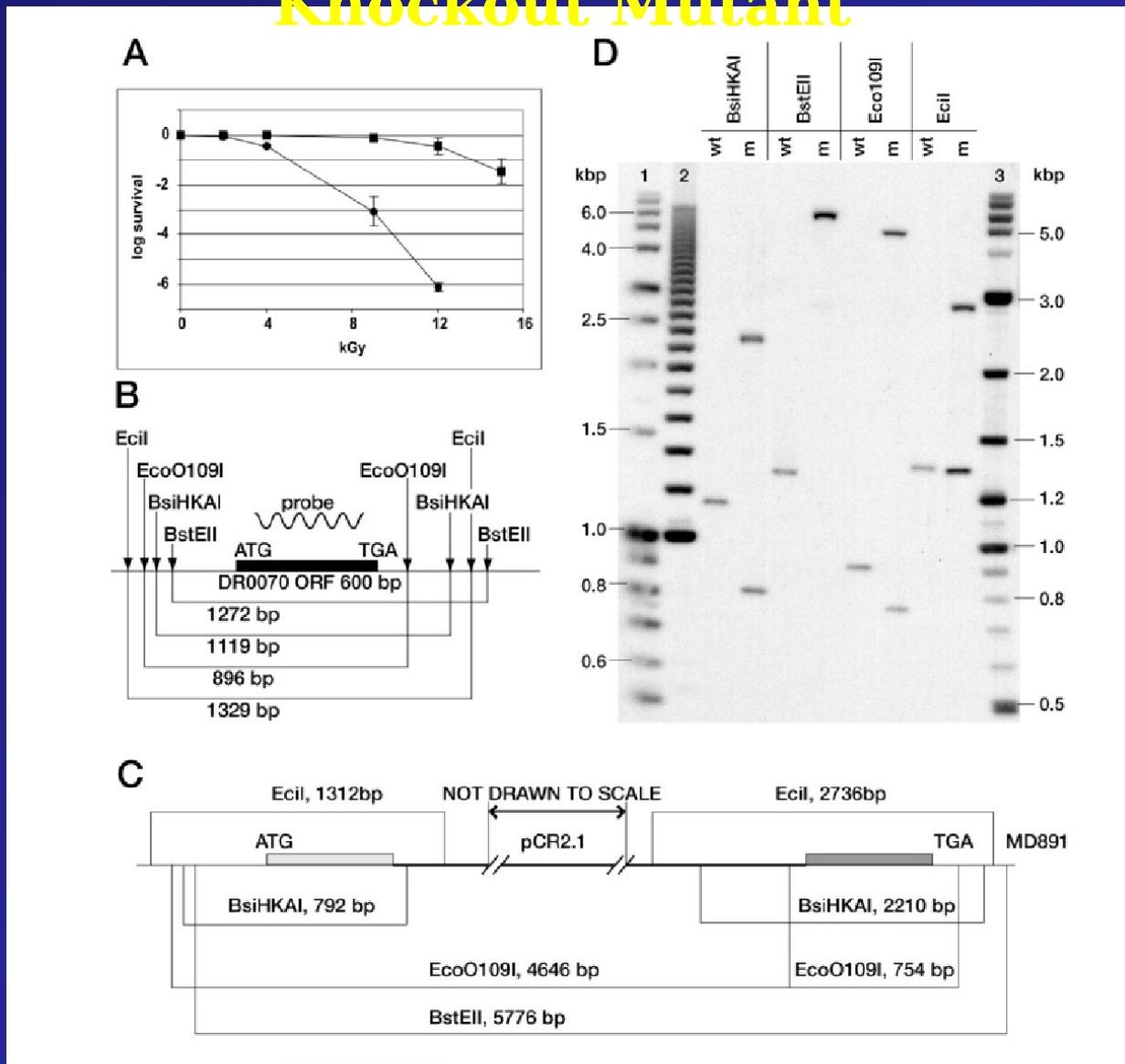
# Coordinated Expression of Genes Belonging to the Same Operon or Multi-Subunit Complex



# Expression Patterns of Predicted Transcriptional Regulators Potentially Involved in the Regulation of *D. radiodurans*' Irradiation-Response



# Resistance Phenotype, Construction, and Genomic Structure for the DR0070 Knockout Mutant

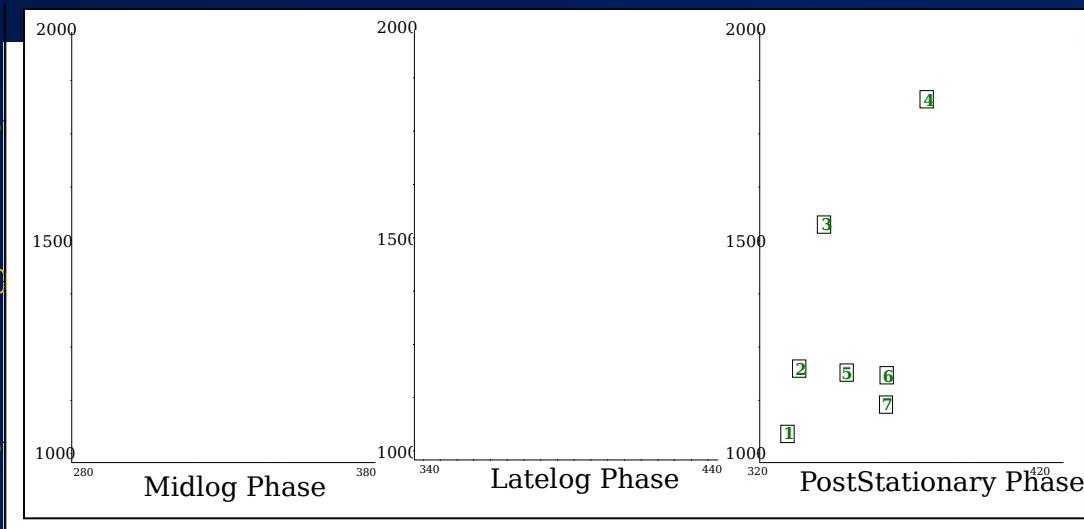


# Different Functional Groups of Genes and Operons of *D. radiodurans* with Early-Mid Expression *recA*-like Patterns and the Result of ORF Disruption

(marked in green)

	Gene_ID <sup>a</sup>	Function group <sup>b</sup>	Protein description and comments	Maximum induction level (fold)	Maximum induction time (hr)	Result of ORF disruption
1	DR0003	-	Uncharacterized protein	14	1.5	m resist to 9 kGy
2	DR0050	L	DinB/YfiT family protein	4	3	
3	DR0051	S	Small cysteine-rich protein of the HesB family	6	3	
4	DR0052	-	Uncharacterized conserved protein	7	1.5	
5	DR0053	L	DinB/YfiT family protein	10	3	m resist to 9 kGy
6	DR0070	ST?	Uncharacterized protein	4	9	m sens to 5 kGy, homozyg
7	DR0103	R	Predicted metal-binding protein	6	1.5	
8	DR0105	ST	LEA76 family desiccation resistance protein	3	0.5	m resist to 9 kGy
9	DR0140	-	Uncharacterized protein	6	1.5	m resist to 9 kGy
10	DR0160	-	Conserved membrane protein	4	1.5	
11	DR0161	S	AmsJ/WcaK related protein, possibly involved in exopolysaccharide biosynthesis	8	1.5	
12	DR0203	R	Uncharacterized membrane protein	4	1.5	
13	DR0204	R	Uncharacterized membrane protein	6	3	

Molecular Weight



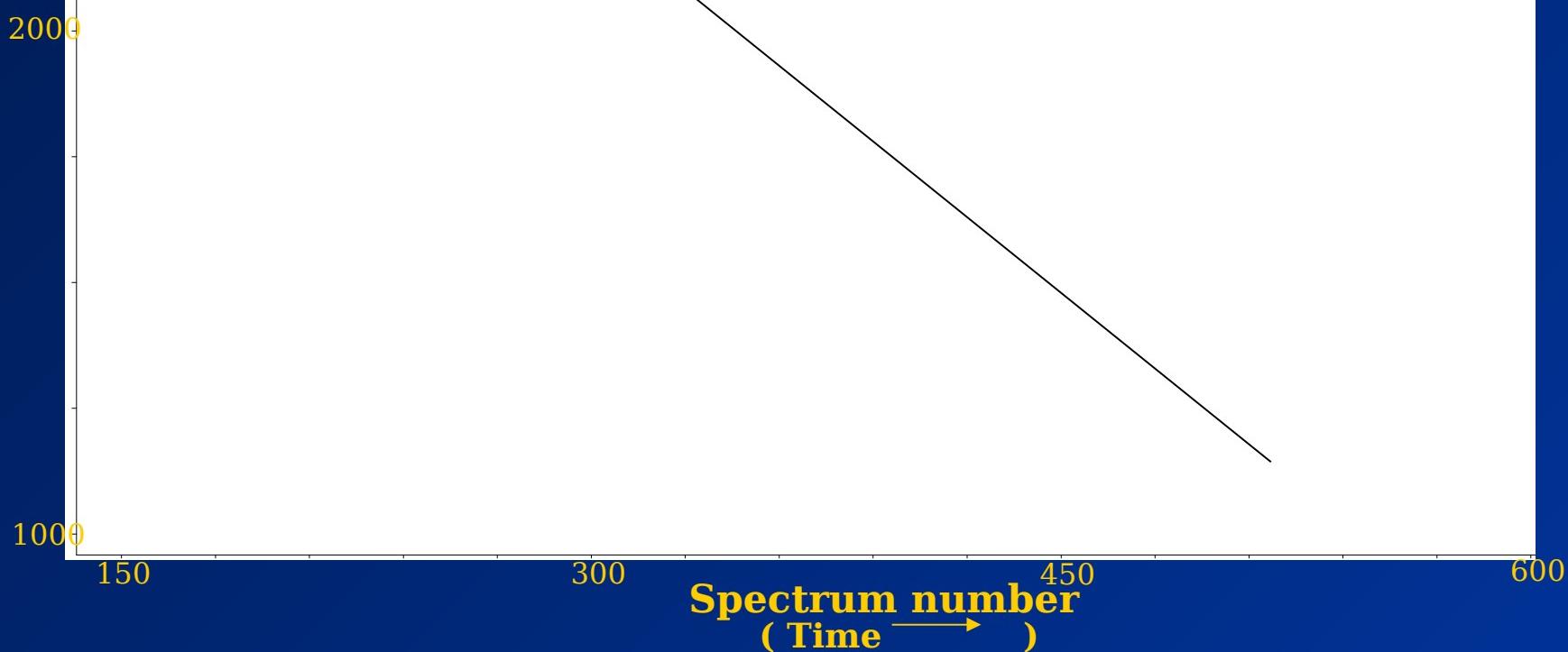
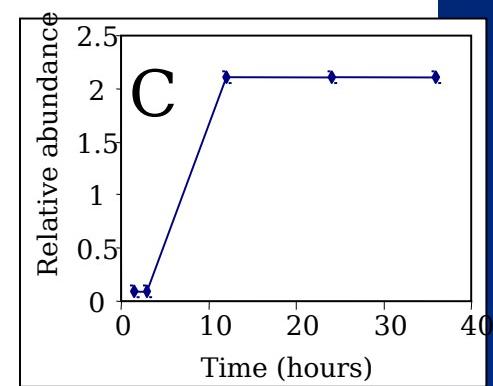
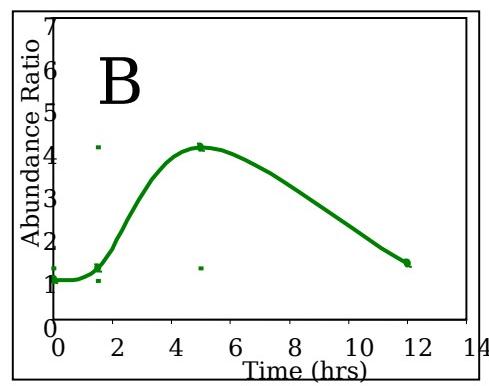
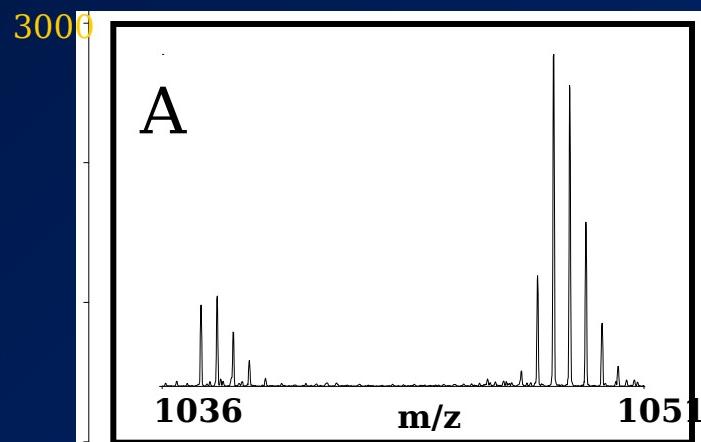
Spectrum number  
(Time →)

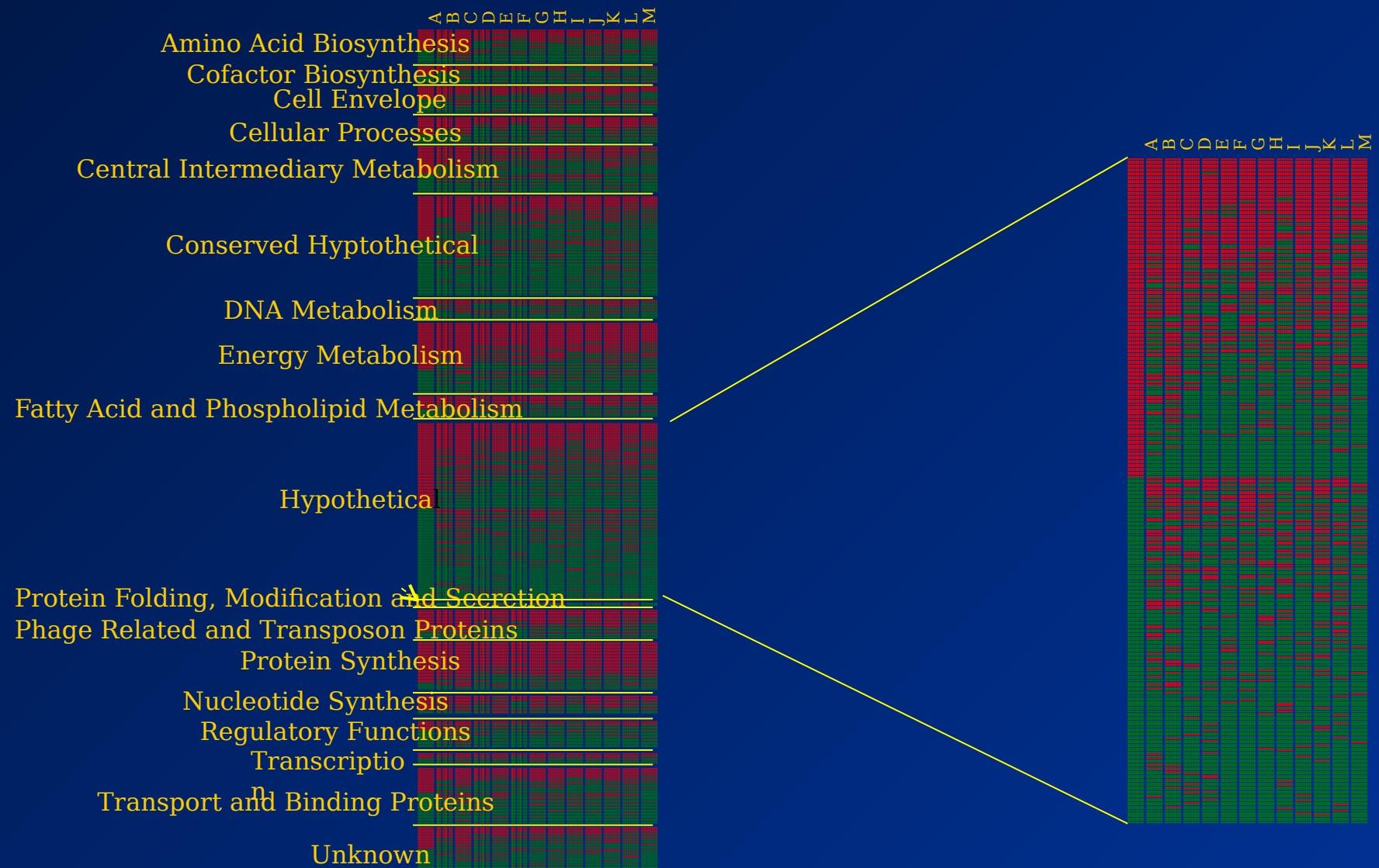
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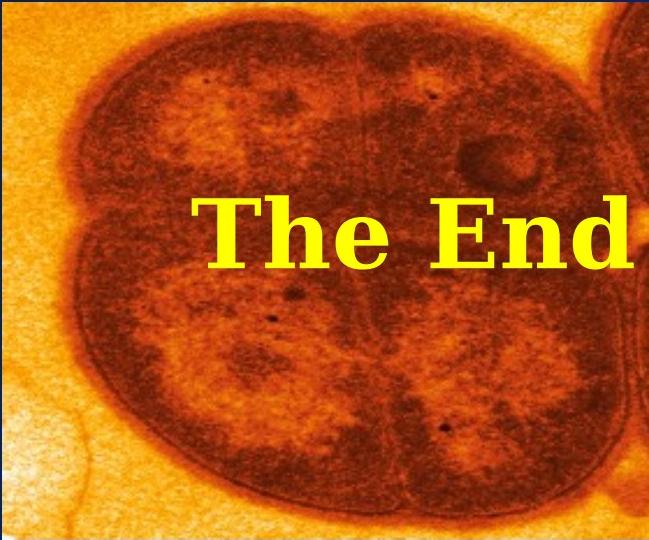
2D display of a capillary LC-FTICR analysis in which >50,000 putative polypeptides were detected from a tryptic digest of proteins isolated from *D. radiodurans* harvested in mid log phase. The inset shows three 2-D displays for peptides isolated from *D. radiodurans* harvested in midlog, late log and post stationary phases. Within the inset, spot size has been adjusted to show highly abundant species as larger spots creating a display similar to that of a 2-D PAGE.

Less abundant      More abundant

Molecular Weight







The End